

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/520,299
Source: PCT
Date Processed by STIC: 01/31/2006

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 01/31/2006

PATENT APPLICATION: US/10/520,299

TIME: 15:48:25

Input Set : E:\HYS-B2 PCT Sequence Listing.txt

Output Set: N:\CRF4\01312006\J520299.raw

3 <110> APPLICANT: Rupp, Fabio
4 Wang, Jianrui
5 Zhou, Ping
6 Wehrman, Tom
7 Wang, Zhiwei
8 Tang, Y. Tom
10 <120> TITLE OF INVENTION: Methods and Materials Relating to Novel Polypeptides and Polynucleotides
12 <130> FILE REFERENCE: HYS-B2 PCT
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/520,299
C--> 15 <141> CURRENT FILING DATE: 2005-01-04
17 <150> PRIOR APPLICATION NUMBER: PCT/US02/29636
18 <151> PRIOR FILING DATE: 2002-09-18
20 <150> PRIOR APPLICATION NUMBER: 60/395,402
21 <151> PRIOR FILING DATE: 2002-07-12
23 <150> PRIOR APPLICATION NUMBER: PCT/US02/22858
24 <151> PRIOR FILING DATE: 2002-07-19
26 <150> PRIOR APPLICATION NUMBER: 10/112,944
27 <151> PRIOR FILING DATE: 2002-03-28
29 <150> PRIOR APPLICATION NUMBER: 60/306,971
30 <151> PRIOR FILING DATE: 2001-07-21
32 <150> PRIOR APPLICATION NUMBER: 10/296,115
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38 <150> PRIOR APPLICATION NUMBER: 09/488,725
39 <151> PRIOR FILING DATE: 2000-01-21
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42 <151> PRIOR FILING DATE: 2002-10-11
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47 <150> PRIOR APPLICATION NUMBER: 60/365,091
48 <151> PRIOR FILING DATE: 2002-03-14
50 <150> PRIOR APPLICATION NUMBER: 60/425,158
51 <151> PRIOR FILING DATE: 2002-11-08
53 <150> PRIOR APPLICATION NUMBER: 60/323,349
54 <151> PRIOR FILING DATE: 2001-09-18
56 <150> PRIOR APPLICATION NUMBER: 09/552,317
57 <151> PRIOR FILING DATE: 2000-04-25
59 <150> PRIOR APPLICATION NUMBER: 10/275,027
60 <151> PRIOR FILING DATE: 2002-10-30
62 <150> PRIOR APPLICATION NUMBER: PCT/US01/02623
63 <151> PRIOR FILING DATE: 2001-01-25
65 <150> PRIOR APPLICATION NUMBER: 09/560,875

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68 <150> PRIOR APPLICATION NUMBER: 10/220,366
69 <151> PRIOR FILING DATE: 2002-08-28
71 <150> PRIOR APPLICATION NUMBER: PCT/US01/04927
72 <151> PRIOR FILING DATE: 2001-02-26
74 <150> PRIOR APPLICATION NUMBER: 09/577,409
75 <151> PRIOR FILING DATE: 2000-05-18
77 <150> PRIOR APPLICATION NUMBER: 09/515,126
78 <151> PRIOR FILING DATE: 2000-02-28
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95 <150> PRIOR APPLICATION NUMBER: 10/276,817
96 <151> PRIOR FILING DATE: 2002-11-18
98 <150> PRIOR APPLICATION NUMBER: 09/491,404
99 <151> PRIOR FILING DATE: 2000-01-25
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102 <151> PRIOR FILING DATE: 2002-10-03
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135 <151> PRIOR FILING DATE: 2001-01-26
137 <150> PRIOR APPLICATION NUMBER: PCT/US01/14827
138 <151> PRIOR FILING DATE: 2001-05-16

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143 <150> PRIOR APPLICATION NUMBER: 10/221,279
144 <151> PRIOR FILING DATE: 2003-05-28
146 <160> NUMBER OF SEQ ID NOS: 110
148 <170> SOFTWARE: PatentIn version 3.1
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151 <211> LENGTH: 1222
152 <212> TYPE: DNA
153 <213> ORGANISM: Homo sapiens
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156 <221> NAME/KEY: misc_feature
157 <222> LOCATION: (392)..(1008)
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164 gccggtgccc cccatgttgg aacctgagtt ggagattatc tcctaagcag atacctgctt      120
166 ccaaactggg gatgtagggc ttggaaacta aaaaatgcc aagttggcag gggtgtgttc      180
168 acaagtccag caatacacag agctctgtgt attcagaggg aagttggcag gggtgtgttc      240
170 gggcagagaa actccgagtg gtacaaaggg gacgtgcccc gagtggagaa atcatgctaa      300
172 ttgtctgcac tagagctgga gaacgccacc caaatgaag agagaaaggg gagccctgtc      360
174 cagagcctcc agggccctgc gccttgctcc ttttgtctac cttcttctga tccagacaga      420
176 ccccttgagg ggggtgaaca tcaccagccc cgtgcgcctg atccatggca ccgtggggaa      480
178 gtcggctctg ctttctgtgc agtacagcag taccagcagc gacaggcctg tagtgaagtg      540
180 gcagctgaag cgggacaagc cagtgaccgt ggtgcagtcc attggcacag aggtcatcgg      600
182 caccctgcgg cctgactatc gggaccgtat ccgactcttt gaaaatggct ccctgcttct      660
184 cagcgacctg cagctggccg atgagggcac ctatgaggtc gagatctcca tcaccgacga      720
186 caccttcact ggggagaaga ccatcaacct tactgtagat gtgcccattt cgaggccaca      780
188 ggtgttgggg gcttcaacca ctgtgctgga gctcagcgag gccttcacct tgaactgctc      840
190 acatgagaat ggcaccaagc ccagctacac ctggctgaag gatggcaagc ccctcctcaa      900
192 tgactcgaga atgctcctgt ccccgacca aaagggtgctc accatcaccg gcgtgctcat      960
194 ggaggatgac gacctgtaca gctgcgtggt ggaaaacccc atcaaccagg gccggaccct      1020
196 gccttgtaag atcaccgaat acagaaaaag ctccctttca tcaatttggc tccaggaggc      1080
198 attttcctcc ttgggacctt ggtgaagacc tggccaacaa gggaaaaccc cgtctttatt      1140
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206 <211> LENGTH: 823
207 <212> TYPE: DNA
208 <213> ORGANISM: Homo sapiens
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211 <221> NAME/KEY: CDS
212 <222> LOCATION: (50)..(817)
213 <223> OTHER INFORMATION:
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218                                     Met Lys Arg
219                                     1
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222 Glu Arg Gly Ala Leu Ser Arg Ala Ser Arg Ala Leu Arg Leu Ala Pro
223   5                               10                               15
225 ttt gtc tac ctt ctt ctg atc cag aca gac ccc ctg gag ggg gtg aac      154
226 Phe Val Tyr Leu Leu Leu Ile Gln Thr Asp Pro Leu Glu Gly Val Asn
227 20                               25                               30                               35
229 atc acc agc ccc gtg cgc ctg atc cat ggc acc gtg ggg aag tcg gct      202
230 Ile Thr Ser Pro Val Arg Leu Ile His Gly Thr Val Gly Lys Ser Ala
231   40                               45                               50
233 ctg ctt tct gtg cag tac agc agt acc agc agc gac agg cct gta gtg      250
234 Leu Leu Ser Val Gln Tyr Ser Ser Thr Ser Ser Asp Arg Pro Val Val
235   55                               60                               65
237 aag tgg cag ctg aag cgg gac aag cca gtg acc gtg gtg cag tcc att      298
238 Lys Trp Gln Leu Lys Arg Asp Lys Pro Val Thr Val Val Gln Ser Ile
239   70                               75                               80
241 ggc aca gag gtc atc ggc acc ctg cgg cct gac tat cga gac cgt atc      346
242 Gly Thr Glu Val Ile Gly Thr Leu Arg Pro Asp Tyr Arg Asp Arg Ile
243   85                               90                               95
245 cga ctc ttt gaa aat ggc tcc ctg ctt ctc agc gac ctg cag ctg gcc      394
246 Arg Leu Phe Glu Asn Gly Ser Leu Leu Leu Ser Asp Leu Gln Leu Ala
247 100                               105                               110                               115
249 gat gag ggc acc tat gag gtc gag atc tcc atc acc gac gac acc ttc      442
250 Asp Glu Gly Thr Tyr Glu Val Glu Ile Ser Ile Thr Asp Asp Thr Phe
251   120                               125                               130
253 act ggg gag aag acc atc aac ctt act gta gat gtg ccc att tcg agg      490
254 Thr Gly Glu Lys Thr Ile Asn Leu Thr Val Asp Val Pro Ile Ser Arg
255   135                               140                               145
257 cca cag gtg ttg gtg gct tca acc act gtg ctg gag ctc agc gag gcc      538
258 Pro Gln Val Leu Val Ala Ser Thr Thr Val Leu Glu Leu Ser Glu Ala
259   150                               155                               160
261 ttc acc ttg aac tgc tca cat gag aat ggc acc aag ccc agc tac acc      586
262 Phe Thr Leu Asn Cys Ser His Glu Asn Gly Thr Lys Pro Ser Tyr Thr
263   165                               170                               175
265 tgg ctg aag gat ggc aag ccc ctc ctc aat gac tcg aga atg ctc ctg      634
266 Trp Leu Lys Asp Gly Lys Pro Leu Leu Asn Asp Ser Arg Met Leu Leu
267 180                               185                               190                               195
269 tcc ccc gac caa aag gtg ctc acc atc acc cgc gtg ctc atg gag gat      682
270 Ser Pro Asp Gln Lys Val Leu Thr Ile Thr Arg Val Leu Met Glu Asp
271   200                               205                               210
273 gac gac ctg gac agc tgc gtg gtg gaa aac ccc atc aac cag ggc cgg      730
274 Asp Asp Leu Asp Ser Cys Val Val Glu Asn Pro Ile Asn Gln Gly Arg
275   215                               220                               225
277 acc ctg cct tgt aag atc acc gta tac aaa aaa agc tcc ttt tac ata      778
278 Thr Leu Pro Cys Lys Ile Thr Val Tyr Lys Lys Ser Ser Phe Tyr Ile
279   230                               235                               240
281 att tgt ctc aag gag gca tct tcc tcc ttt gga cct tgg tgaaga      823
282 Ile Cys Leu Lys Glu Ala Ser Ser Ser Phe Gly Pro Trp
283   245                               250                               255
286 <210> SEQ ID NO: 3
287 <211> LENGTH: 1245

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288 <212> TYPE: DNA

289 <213> ORGANISM: Homo sapiens

291 <220> FEATURE:

292 <221> NAME/KEY: CDS

293 <222> LOCATION: (335)..(1147)

294 <223> OTHER INFORMATION:

W--> 297 <400> 3

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302 ccaaactggg gatgtagggc ttggaaacta gaaaatgcca ggtctgaggg agaggaaaga      180
304 acaagtccag caatacacag agctctgtgt attcagaggg aagttggcag ggttgtgttc      240
306 gggcagagaa actccgagtg gtacaaaggg gacgtgcccc gagtggagaa atcatgctaa      300
308 ttgtctgcac tagagctgga gaacgccacc caaa atg aag aga gaa agg gga gcc      355
309                                     Met Lys Arg Glu Arg Gly Ala
310                                     1                               5
312 ctg tcc aga gcc tcc agg gcc ctg cgc ctt gct cct ttt gtc tac ctt      403
313 Leu Ser Arg Ala Ser Arg Ala Leu Arg Leu Ala Pro Phe Val Tyr Leu
314          10                      15                      20
316 ctt ctg atc cag aca gac ccc ctg gag ggg gtg aac atc acc agc ccc      451
317 Leu Leu Ile Gln Thr Asp Pro Leu Glu Gly Val Asn Ile Thr Ser Pro
318      25                      30                      35
320 gtg cgc ctg atc cat ggc acc gtg ggg aag tcg gct ctg ctt tct gtg      499
321 Val Arg Leu Ile His Gly Thr Val Gly Lys Ser Ala Leu Leu Ser Val
322 40                      45                      50                      55
324 cag tac agc agt acc agc agc gac agg cct gta gtg aag tgg cag ctg      547
325 Gln Tyr Ser Ser Thr Ser Ser Asp Arg Pro Val Val Lys Trp Gln Leu
326          60                      65                      70
328 aag cgg gac aag cca gtg acc gtg gtg cag tcc att ggc aca gag gtc      595
329 Lys Arg Asp Lys Pro Val Thr Val Val Gln Ser Ile Gly Thr Glu Val
330          75                      80                      85
332 atc ggc acc ctg cgg cct gac tat cga gac cgt atc cga ctc ttt gaa      643
333 Ile Gly Thr Leu Arg Pro Asp Tyr Arg Asp Arg Ile Arg Leu Phe Glu
334          90                      95                      100
336 aat ggc tcc ctg ctt ctc agc gac ctg cag ctg gcc gat gag ggc acc      691
337 Asn Gly Ser Leu Leu Leu Ser Asp Leu Gln Leu Ala Asp Glu Gly Thr
338      105                      110                      115
340 tat gag gtc gag atc tcc atc acc gac gac acc ttc act ggg gag aag      739
341 Tyr Glu Val Glu Ile Ser Ile Thr Asp Asp Thr Phe Thr Gly Glu Lys
342 120                      125                      130                      135
344 acc atc aac ctt act gta gat gtg ccc att tcg agg cca cag gtg ttg      787
345 Thr Ile Asn Leu Thr Val Asp Val Pro Ile Ser Arg Pro Gln Val Leu
346          140                      145                      150
348 gtg gct tca acc act gtg ctg gag ctc agc gag gcc ttc acc ttg aac      835
349 Val Ala Ser Thr Thr Val Leu Glu Leu Ser Glu Ala Phe Thr Leu Asn
350          155                      160                      165
352 tgc tca cat gag aat ggc acc aag ccc agc tac acc tgg ctg aag gat      883
353 Cys Ser His Glu Asn Gly Thr Lys Pro Ser Tyr Thr Trp Leu Lys Asp
354          170                      175                      180
356 ggc aag ccc ctc ctc aat gac tcg aga atg ctc ctg tcc ccc gac caa      931

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:15; Xaa Pos. 2,3
Seq#:16; Xaa Pos. 4,5,7,8
Seq#:17; N Pos. 676,724,742,755,769,824
Seq#:38; N Pos. 1096,1123
Seq#:106; Xaa Pos. 3,4

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 10

VERIFICATION SUMMARY

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L:14 M:270 C: Current Application Number differs, Replaced Current Application Number
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:161 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:158
L:216 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:213
L:297 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:294
L:592 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:589
L:1240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:1260 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:1281 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:1272
L:1324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:618
M:341 Repeated in SeqNo=17
L:1448 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:1445
L:1606 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:25,Line#:1603
L:1776 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:1773
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L:4829 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:96,Line#:4826
L:5290 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:106 after pos.:0